Amendment to the Claims:

Please amend the claims as follows:

Please cancel claims 2 to 36, 38 to 43, 45, 46, 48 to 60, 62 to 64, 66 to 71, 73, 74, 76 to 98, 100 to 105, 109 to 111, 113, 115, 117, 120, 121, 123 to 128, 130 to 139, 141 to 143, 145 to 149, 151 to 154, 156 to 177, 179 to 203, 207, 208, 210 to 212, 214, 215, 217 to 221, 223, 225 to 228, 230 to 234, 236 to 238 without prejudice or disclaimer.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): An isolated, synthetic or recombinant nucleic acid comprising:

(a) a nucleic acid sequence having at least 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to SEQ ID NO:1 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, wherein the nucleic acid encodes a polypeptide having a xylose isomerase activity; or

(b) a nucleic acid sequence having at least 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to SEQ ID NO:3 over a region of at least about 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, wherein the nucleic acid encodes a polypeptide having a xylose isomerase activity; or

(c) a nucleic acid sequence encoding a polypeptide having a xylose isomerase activity comprising the sequence or SEQ ID NO:2, or SEQ ID NO:4, or enzymatically active fragments thereof; or

(d) a nucleic acid sequence that hybridizes under stringent conditions to a nucleic acid comprising the sequence or SEQ ID NO:1, or SEQ ID NO:3, wherein the nucleic acid encodes a polypeptide having a xylose isomerase activity, wherein the sequence is at least about 25, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues in length, or the full length of a gene or a transcript,

wherein optionally the stringent conditions comprise a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes; or

(e) a nucleic acid sequence completely complementary to (a), (b), (c) or (d),

wherein the nucleic acid encodes at least one polypeptide having a xylose isomerase activity, and optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection,

and optionally the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default,

and optionally the xylose isomerase activity comprises: isomerization of xylose to xylulose; isomerization of glucose to fructose; isomerization of D-glucose to D-fructose; catalysis of the conversion of D-xylose to an equilibrium mixture of D-xylulose and D-xylose; isomerization of α-D-glucopyranose to α-D-fructofuranose; isomerization of β-D-glucopyranose to β-D-fructopyranose,

and optionally the xylose isomerase activity is thermostable, and optionally the polypeptide retains a xylose isomerase activity under conditions comprising a temperature range of between about 60°C to about 120°C, or, between about 60°C to about 95°C, or retains a xylose isomerase activity under conditions comprising a temperature range of between about 95°C to about 105°C, or, between about 105°C to about 120°C,

and optionally the xylose isomerase activity thermotolerant, and optionally retains a xylose isomerase activity after exposure to conditions comprising a temperature range of between about 95°C to about 135°C, or, between about 95°C to about 105°C, or between about 105°C to about 120°C, or, between about 120°C to about 135°C.

Claims 2 to 36 (canceled)

Claim 37 (currently amended): A nucleic acid probe for identifying, detecting or isolating a nucleic acid encoding a polypeptide comprising a xylose isomerase activity, wherein the probe comprises at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more consecutive bases of a sequence comprising: (a) the sequence of claim 1; or,

(b) the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:1, or

~~a sequence as set forth in~~ SEQ ID NO:3,

wherein the probe identifies, detects or isolates the nucleic acid by binding or hybridization,

wherein optionally the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases.

Claims 38 to 43 (canceled)

Claim 44 (currently amended): An amplification primer ~~sequence~~ pair for amplifying a nucleic acid encoding a polypeptide having a xylose isomerase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising (a) the sequence of claim 1; or,

(b) the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:1 or SEQ ID NO:3 ~~or subsequences thereof~~,

wherein optionally each member of the amplification primer ~~sequence~~ pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence of (a) or (b), or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence of (a) or (b),

or optionally the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of (a) or (b), and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the complementary strand of the first member.

Claims 45 to 46 (canceled)

Claim 47 (currently amended): An expression cassette, a vector or a cloning vehicle comprising the [[a]] nucleic acid of claim 1 ~~comprising:~~

~~(i) a nucleic acid sequence having at least 96% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 or SEQ ID NO:3 or subsequences thereof,~~

wherein optionally the nucleic acid is operably linked to a plant promoter, a potato promoter, a rice promoter, a corn promoter, a wheat promoter or a barley promoter, a promoter derived from T-DNA of *Agrobacterium tumefaciens*, a constitutive promoter, an inducible promoter, a tissue-specific promoter, a seed-specific, a leaf-specific, a root-specific, a stem-specific or an abscission-induced promoter,

and optionally the expression cassette, vector or cloning vehicle comprises or further comprises a plant expression vector or a plant virus,

and optionally the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome, and optionally the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector, and optionally the cloning vehicle comprises a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

Claims 48 to 60 (canceled)

Claim 61 (currently amended): A transformed cell comprising the [[a]] vector, expression cassette or a cloning vehicle of claim 47, or the nucleic acid of claim 1, ~~wherein the vector comprises~~

~~(i) a nucleic acid sequence having at least 96% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 or SEQ ID NO:3 or subsequences thereof~~

wherein optionally the cell is a bacterial cell, a mammalian cell , a fungal cell, a yeast cell, an insect cell or a plant cell, and optionally the plant cell is a potato, rice, corn, wheat, tobacco, rapeseed, grass, soybean or barley cell.

Claims 62 to 64 (canceled)

Claim 65 (currently amended): A transgenic non-human animal or transgenic plant or seed comprising

the **[[**(i) a**]]** nucleic acid sequence of claim 1, or the vector, expression cassette or a cloning vehicle of claim 47, ~~having at least 96% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 or SEQ ID NO:3 or subsequences thereof~~

wherein optionally the animal is a mouse,

and optionally the plant is a corn plant, a potato plant, a grass, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant or a tobacco plant,

and optionally the seed is a starch granule or grain, corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a peanut or a tobacco plant seed.

Claims 66 to 71 (canceled)

Claim 72 (currently amended): An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to

the [[(i) a]] nucleic acid sequence of claim 1, ~~having at least 96% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 or SEQ ID NO:3 or subsequences thereof~~

wherein optionally the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

Claims 73 to 74 (canceled)

Claim 75 (currently amended): An isolated, synthetic or recombinant polypeptide comprising

(a) a polypeptide comprising

an amino acid sequence having at least 96%, 97%, 98%, 99%, or more, or complete (100%) identity to SEQ ID NO:2 over a region of at least about 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350 or more residues, or over the full length of the polypeptide, or

an amino acid sequence having at least 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) identity to SEQ ID NO:4 over a region of at least about 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350 or more residues, or over the full length of the polypeptide, or

(b) a polypeptide encoded by the [[a]] nucleic acid of claim 1;

(c) the polypeptide of (a) or (b) lacking a signal sequence; or

(d) the polypeptide of (a), (b) or (c) comprising a heterologous signal sequence or catalytic domain (CD), wherein optionally the signal sequence comprises a heterologous xylose isomerase or non-xylose isomerase signal sequence,

~~(i) a nucleic acid sequence having at least 96% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1 or SEQ ID NO:3 or subsequences thereof~~

wherein the nucleic acid encodes at least one polypeptide having a xylose isomerase activity, and optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection,

and optionally the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default,

and optionally the xylose isomerase activity comprises: isomerization of xylose to xylulose; isomerization of glucose to fructose; isomerization of D-glucose to D-fructose; catalysis of the conversion of D-xylose to an equilibrium mixture of D-xylulose and D-xylose; isomerization of α-D-glucopyranose to α-D-fructofuranose; isomerization of β-D-glucopyranose to β-D-fructopyranose,

and optionally the xylose isomerase activity is thermostable, and optionally the polypeptide retains a xylose isomerase activity under conditions comprising a temperature range of between about 60°C to about 120°C, or, between about 60°C to about 95°C, or retains a xylose isomerase activity under conditions comprising a temperature range of between about 95°C to about 105°C, or, between about 105°C to about 120°C,

and optionally the xylose isomerase activity thermotolerant, and optionally retains a xylose isomerase activity after exposure to conditions comprising a temperature range of between about

95°C to about 135°C, or, between about 95°C to about 105°C, or between about 105°C to about 120°C, or, between about 120°C to about 135°C,

and optionally the xylose isomerase activity comprises a specific activity at about 95°C in the range from about 100 to about 1000 units per milligram of protein, or, a specific activity from about 500 to about 750 units per milligram of protein, or, a specific activity at 95°C in the range from about 500 to about 1200 units per milligram of protein, or, a specific activity at 95°C in the range from about 750 to about 1000 units per milligram of protein,

and optionally the polypeptide comprises at least one glycosylation site, and optionally the glycosylation is an N-linked glycosylation, and optionally the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*,

and optionally the polypeptide retains a xylose isomerase activity under conditions comprising about pH 4.0, 4.5, 5.0, 5.5, 6.0 or 6.5, or the polypeptide retains a xylose isomerase activity under conditions comprising about pH 8.0, 8.5, 9.0, 9.5, 10, 10.5 or 11.

Claims 76 to 98 (canceled)

Claim 99 (currently amended): An isolated, synthetic or recombinant signal sequence peptide comprising a sequence as set forth in the amino terminal 20 to 30 residues of (a) the polypeptide of claim 75, or (b) the polypeptide having the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4.

Claims 100 to 105 (canceled)

Claim 106 (original): A protein preparation comprising a polypeptide as set forth in claim 75, wherein the protein preparation comprises a liquid, a solid or a gel.

Claim 107 (original): A homodimer comprising a polypeptide as set forth in claim 75.

Claim 108 (currently amended): A heterodimer comprising a polypeptide as set forth in claim 75 and a second domain, wherein optionally the second domain is a polypeptide and the heterodimer is a fusion protein, or the second domain is an epitope or a tag.

Claims 109 to 111 (canceled)

Claim 112 (currently amended): An immobilized polypeptide having a xylose isomerase activity, wherein the polypeptide comprises a sequence as set forth in claim 75 or claim 108, wherein optionally the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

Claim 113 (canceled)

Claim 114 (currently amended): An array comprising an immobilized polypeptide asset forth in claim 75 or claim 108, or an immobilized nucleic acid asset forth in claim 1.

Claim 115 (canceled)

Claim 116 (currently amended): An isolated or recombinant antibody that specifically binds to the [[a]] polypeptide of ~~as set forth in~~ claim 75 or to a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein optionally the antibody is a monoclonal or a polyclonal antibody.

Claim 117 (canceled)

Claim 118 (currently amended): A hybridoma comprising an antibody that specifically binds to the [[a]] polypeptide of ~~as set forth in~~ claim 75 or to a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~.

Claim 119 (currently amended): A food supplement for an animal comprising the [[a]] polypeptide of ~~as set forth in~~ claim 75 or to a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~,

wherein optionally the polypeptide is glycosylated, or the food supplement comprises a glucose or a starch.

Claims 120 to 121 (canceled)

Claim 122 (currently amended): An edible enzyme delivery matrix comprising the [[a]] polypeptide of ~~as set forth in~~ claim 75 or to a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein optionally the polypeptide comprises a xylose isomerase activity, or the edible enzyme delivery matrix comprises a glucose or a starch, or the delivery matrix comprises a pellet, or the polypeptide is glycosylated, or the xylose isomerase activity is thermotolerant or thermostable.

Claims 123 to 128 (canceled)

Claim 129 (currently amended): A method of producing a recombinant polypeptide comprising the steps of

(a) providing a nucleic acid operably linked to a promoter; wherein the nucleic acid comprises the nucleic acid [[a]] sequence of ~~as set forth in~~ claim 1 ~~or claim 30~~; and

(b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide,

and optionally the method further comprises transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell, and optionally the cell is a plant cell.

Claims 130 to 139 (canceled)

Claim 140 (currently amended): A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises the sequence of ~~as set forth in~~ claim 75, or subsequence thereof, and the nucleic acid comprises the nucleic acid [[a]] sequence of ~~as set forth in~~ claim 1 ~~or claim 30~~, or subsequence thereof,

and optionally the computer system further comprises a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon, or optionally the sequence comparison algorithm comprises a computer program that indicates polymorphisms, or optionally the computer system further comprises an identifier that identifies one or more features in said sequence.

Claims 141 to 143 (canceled)

Claim 144 (currently amended): A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises the sequence of ~~as set forth in~~ claim 75, or subsequence thereof, and the nucleic acid comprises the nucleic acid [[a]] sequence of ~~as set forth in~~ claim 1 ~~or claim 30~~, or subsequence thereof.

Claims 145 to 149 (canceled)

Claim 150 (currently amended): A method for isolating, detecting or recovering a nucleic acid encoding a polypeptide with a xylose isomerase activity from a ~~an environmental~~ sample comprising the steps of:

(A) (a) providing an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide with a xylose isomerase activity, wherein the primer pair is capable of amplifying SEQ ID NO:1 or SEQ ID NO:3, or a subsequence thereof, or the sequence of claim 1;

(b) isolating a nucleic acid from the ~~environmental~~ sample or treating the ~~environmental~~ sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the ~~environmental~~ sample, thereby isolating, detecting or recovering a nucleic acid encoding a polypeptide with a xylose isomerase activity from a ~~an environmental~~ sample; or,

(B) (a) providing a polynucleotide probe comprising the sequence of claim 1, or the probe sequence of claim 37;

(b) isolating a nucleic acid from the sample or treating the sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating, detecting or recovering a nucleic acid encoding a polypeptide with a xylose isomerase activity from the sample,

wherein optionally the sample comprises an environmental sample, and optionally each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, or a subsequence thereof,

and optionally the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample, and optionally the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

Claims 151 to 154 (canceled)

Claim 155 (currently amended): A method of generating a variant of a nucleic acid encoding a polypeptide with a xylose isomerase activity comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 30; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid,

wherein optionally the method further comprises expressing the variant nucleic acid to generate a variant xylose isomerase polypeptide, or optionally the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturation mutagenesis (GSSM), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation, or a combination thereof,

and optionally the method is iteratively repeated until a xylose isomerase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced, or optionally the variant xylose isomerase polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature, or optionally the variant xylose isomerase polypeptide has increased glycosylation as compared to the xylose isomerase encoded by a template nucleic acid, or optionally the variant xylose isomerase polypeptide has a xylose isomerase activity under a high temperature, wherein the xylose isomerase encoded by the template nucleic acid is not active under the high temperature,

and optionally the method is iteratively repeated until a xylose isomerase coding sequence having an altered codon usage from that of the template nucleic acid is produced,

and optionally the method is iteratively repeated until a xylose isomerase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

Claims 156 to 177 (canceled)

Claim 178 (currently amended): A method for modifying codons in a nucleic acid encoding a polypeptide with a xylose isomerase activity to increase its expression in a host cell, the method comprising the following steps:

(A) (a) providing a nucleic acid encoding a polypeptide with a xylose isomerase activity comprising the nucleic acid [[a]] sequence of ~~as set forth in~~ claim 1 ~~or claim 30~~, or a nucleic acid encoding the polypeptide of claim 75; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell, or

(B) (a) providing a nucleic acid encoding a polypeptide with a xylose isomerase activity comprising the sequence of claim 1, or a nucleic acid encoding the polypeptide of claim 75; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a xylose isomerase,

wherein optionally the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

Claims 179 to 203 (canceled)

Claim 204 (currently amended): A kit comprising the [[a]] polypeptide of ~~as set forth in~~ claim 75 or a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein the polypeptide comprises a xylose isomerase activity.

Claim 205 (currently amended): A method for catalyzing the isomerization of a glucose to a fructose comprising the following steps:

(a) providing the [[a]] polypeptide of ~~as set forth in~~ claim 75 or a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein the polypeptide comprises a xylose isomerase activity;

(b) providing a composition comprising a glucose; and

(c) contacting the polypeptide of step (a) with the glucose of step (b) under conditions wherein the polypeptide of step (a) can isomerase the glucose to a fructose, thereby producing a fructose.

Claim 206 (currently amended): A method for producing fructose from a starch comprising the following steps:

(a) providing a polypeptide capable of hydrolyzing a α-1,4-glycosidic linkage in a starch;

(b) contacting the polypeptide of the step (a) with the starch under condition wherein the polypeptide of step (a) can hydrolyze α-1,4-glycosidic linkages in the starch,

(c) providing the [[a]] polypeptide of ~~as set forth in~~ claim 75 or a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein the polypeptide comprises a xylose isomerase activity; and

(d) contacting the polypeptide of step (c) with the glucose of step (b) under conditions wherein the polypeptide of step (c) can isomerase glucose, thereby producing fructose,

wherein optionally the polypeptide of step (a) comprises an xylose isomerase or a glucoamylase, and optionally step (a) further comprises or comprises a polypeptide capable of hydrolyzing α-1,6-glycosidic linkage in a starch.

Claims 207 to 208 (canceled)

Claim 209 (currently amended): A method for producing fructose comprising the following steps:

(a) providing a glucose;

(b) providing a polypeptide having a xylose isomerase activity, wherein the polypeptide comprises the [[a]] amino acid sequence of ~~as set forth in~~ claim 75, or, a polypeptide encoded by the [[a]] nucleic acid ~~having a~~ sequence of ~~as set forth in~~ claim 1 ~~or claim 30~~; and

(c) contacting the polypeptide of step (b) with the glucose of step (a) under conditions wherein the polypeptide can isomerase glucose thereby producing fructose,

wherein optionally the conditions comprise a temperature of between about 70°C and 95°C, thereby shifting equilibrium of the reaction towards formation of fructose, and optionally the conditions comprise a temperature of between about 80°C and 90°C, thereby shifting equilibrium of the reaction towards formation of fructose, and optionally the polypeptide of step (b) is immobilized.

Claims 210 to 212 (canceled)

Claim 213 (currently amended): A method of making fructose in a feed or a food prior comprising the following steps:

(a) obtaining a feed or a food material comprising a starch,

(b) providing a polypeptide capable of hydrolyzing a α-1,4- glycosidic linkage in a starch;

(c) contacting the polypeptide of the step (a) with the feed or a food material under conditions wherein the polypeptides of step (a) can hydrolyze α-1,4- glycosidic linkages in the starch to produce a glucose;

(d) providing the [[a]] polypeptide of ~~as set forth in~~ claim 75 or a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein the polypeptide comprises a xylose isomerase activity; and

(e) adding the polypeptide of step (d) to the feed or food material in an amount sufficient to cause isomerization of the glucose to a fructose in the food or the feed,

wherein optionally the food or feed comprises rice, corn, barley, wheat, legumes, or potato, and optionally step (a) further comprises a polypeptide capable of hydrolyzing α-1,6-glycosidic linkage in a starch.

Claims 214 to 215 (canceled)

Claim 216 (currently amended): A method for producing a high-fructose syrup comprising the following steps:

(a) providing a polypeptide capable of hydrolyzing α-1,4- glycosidic linkages in a starch;

(b) providing a composition comprising a starch

(c) contacting the polypeptides of step (a) and the composition of step (b) under conditions wherein the polypeptide of step (a) can hydrolyze α-1,4- glycosidic linkages in the starch;

(d) providing the [[a]] polypeptide of ~~as set forth in~~ claim 75 or a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein the polypeptide comprises a xylose isomerase activity; and

(e) contacting the polypeptide of step (d) and the starch hydrolysate of step (c) under conditions wherein the polypeptide of step (d) can isomerase glucose in the starch hydrolysate to a fructose, thereby producing the high-fructose syrup,

wherein optionally the composition comprises a rice, a corn, a barley, a wheat, a legume, a potato or a sweet potato, and optionally the composition comprises a rice and the high-fructose syrup is a high-fructose corn syrup, and optionally step (a) further comprises a polypeptide capable of hydrolyzing α-1,6-glycosidic linkage in a starch, and optionally all reactions are carried out in one vessel, and optionally the high-fructose syrup comprises an insecticide bait composition.

Claims 217 to 221 (canceled)

Claim 222 (currently amended): A method for producing a high-fructose syrup comprising the following steps:

(a) providing a transgenic seed or grain comprising the [[a]] polypeptide of ~~as set forth in~~ claim 75 or a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, comprising a xylose isomerase activity, wherein the seed or grain comprises a starch;

(b) expressing the xylose isomerase in the seed or grain;

(c) hydrolyzing the starch to a glucose under conditions wherein the polypeptide of step (a) expressed in the seed or grain can catalyze isomerization of glucose to a fructose, thereby producing the high-fructose syrup,

wherein optionally the steps of hydrolyzing the starch and isomerizing the glucose are carried out at pH 4.0 to 6.5 and at temperature comprising a range of about 55°C to 105°C.

Claims 223 (canceled)

Claim 224 (currently amended): A method for producing fructose in brewing or alcohol production comprising the following steps:

(a) providing the [[a]] polypeptide of ~~as set forth in~~ claim 75 or a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein the polypeptide comprises a xylose isomerase activity;

(b) providing malt or mash composition comprising a glucose; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide of step (a) isomerizes the glucose of step (b) to a fructose, thereby producing fructose for brewing or alcohol production.

Claims 225 to 228 (canceled)

Claim 229 (currently amended): A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 30~~, wherein optionally the RNAi is about 15, 16, 17, 18, 19, 20, 2-1, 22, 23, 24, 25 or more duplex nucleotides in length.

Claims 230 to 234 (canceled)

Claim 235 (currently amended): A recombinant xylose isomerase-encoding nucleic acid generated by amplification of the [[a]] polynucleotide of claim 1 using the [[an]] amplification

primer pair of ~~as set forth in~~ claim [[234]] 44, wherein optionally the amplification is by polymerase chain reaction (PCR), or optionally the nucleic acid generated by amplification of a gene library, or optionally the gene library is an environmental library.

Claims 236 to 238 (canceled)

Claim 239 (currently amended): An isolated, synthetic or recombinant protease encoded by the [[a]] xylose isomerase-encoding nucleic acid sequence of ~~as set forth in~~ claim 235.